



SEQUENCE LISTING

<110> CHANG, Y-H
VETRO, J.A.
MICKA, W.S.

<120> DOMINANT NEGATIVE VARIANTS OF METHIONINE AMINOPEPTIDASE
2 ("METAP2") AND CLINICAL USES THEREFOR

<130> 2790/66153/8007

<140> 10/712,359
<141> 2003-11-13

<150> 09/943,123
<151> 2001-08-30

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<170> PatentIn Ver. 3.2

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Lys Lys Lys Lys Lys Lys Lys
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Ser Ala Ala Gly Glu Gln Glu Pro Asp Lys Glu Ser Gly Ala Ser Val 60
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Asp Glu Val Ala Arg Gln Leu Glu Arg Ser Ala Leu Glu Asp Lys Glu 80
65 70 75
Arg Asp Glu Asp Asp Glu Asp Gly Asp Gly Asp Gly Ala Thr 95
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Gly Lys Lys Lys Lys Lys Lys Lys Lys Arg Gly Pro Lys Val Gln 110
100 105
Thr Asp Pro Pro Ser Val Pro Ile Cys Asp Leu Tyr Pro Asn Gly Val 125
115 120
Phe Pro Lys Gly Gln Glu Cys Glu Tyr Pro Pro Thr Gln Asp Gly Arg 140
130 135
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145 150 155
Ala Ser Glu Glu Ile Trp Asn Asp Phe Arg Glu Ala Ala Glu Ala His 175
165 170
Arg Gln Val Arg Lys Tyr Val Met Ser Trp Ile Lys Pro Gly Met Thr 190
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Met Ile Glu Ile Cys Glu Lys Leu Glu Asp Cys Ser Arg Lys Leu Ile 205
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Lys Glu Asn Gly Leu Asn Ala Gly Leu Ala Xaa Pro Thr Gly Cys Ser 220
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Leu Asn Asn Cys Ala Ala Xaa Tyr Thr Pro Asn Ala Gly Asp Thr Thr 240
225 230 235
Val Leu Gln Tyr Asp Asp Ile Cys Lys Ile Xaa Phe Gly Thr His Ile 255
245 250

Ser Gly Arg Ile Ile Xaa Cys Ala Phe Thr Val Thr Phe Asn Pro Lys
 260 265 270
 Tyr Asp Thr Leu Leu Lys Ala Val Lys Asp Ala Thr Asn Thr Gly Ile
 275 280 285
 Lys Cys Ala Gly Ile Asp Val Arg Leu Cys Asp Val Gly Glu Ala Ile
 290 295 300
 Gln Glu Val Met Glu Ser Tyr Glu Val Glu Ile Asp Gly Lys Thr Tyr
 305 310 315 320
 Gln Val Lys Pro Ile Arg Asn Xaa Asn Gly Xaa Ser Ile Gly Gln Tyr
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 Arg Xaa Xaa Ala Gly Lys Thr Val Pro Ile Val Lys Gly Gly Glu Ala
 340 345 350
 Thr Arg Met Glu Glu Gly Glu Val Tyr Ala Ile Xaa Thr Phe Gly Ser
 355 360 365
 Thr Gly Lys Gly Val Val His Asp Asp Met Glu Cys Ser His Tyr Met
 370 375 380
 Lys Asn Phe Asp Val Gly His Val Pro Ile Arg Leu Pro Arg Thr Lys
 385 390 395 400
 His Leu Leu Asn Val Ile Asn Glu Asn Phe Gly Thr Leu Ala Phe Cys
 405 410 415
 Arg Arg Trp Leu Asp Arg Leu Gly Glu Ser Lys Tyr Leu Met Ala Leu
 420 425 430
 Lys Asn Leu Cys Asp Leu Gly Ile Val Asp Pro Xaa Pro Pro Xaa Cys
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 35 40 45
 Val Ser Ala Val Gln Gln Glu Leu Asp Lys Glu Ser Gly Ala Leu Val
 50 55 60
 Asp Glu Val Ala Lys Gln Leu Glu Ser Gln Ala Leu Glu Glu Lys Glu
 65 70 75 80
 Arg Asp Asp Asp Asp Glu Asp Gly Asp Gly Asp Ala Asp Gly Ala Thr
 85 90 95
 Gly Lys Lys Lys Lys Lys Lys Lys Lys Lys Arg Gly Pro Lys Val Gln
 100 105 110
 Thr Asp Pro Pro Ser Val Pro Ile Cys Asp Leu Tyr Pro Asn Gly Val
 115 120 125
 Phe Pro Lys Gly Gln Glu Cys Glu Tyr Pro Pro Thr Gln Asp Gly Arg
 130 135 140
 Thr Ala Ala Trp Arg Thr Thr Ser Glu Glu Lys Lys Ala Leu Asp Gln
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 165 170 175
 Arg Gln Val Arg Lys Tyr Val Met Ser Trp Ile Lys Pro Gly Met Thr
 180 185 190
 Met Ile Glu Ile Cys Glu Lys Leu Glu Asp Cys Ser Arg Lys Leu Ile
 195 200 205
 Lys Glu Asn Gly Leu Asn Ala Gly Leu Ala Xaa Pro Thr Gly Cys Ser
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 Leu Asn Asn Cys Ala Ala Xaa Tyr Thr Pro Asn Ala Gly Asp Thr Thr
 225 230 235 240
 Val Leu Gln Tyr Asp Asp Ile Cys Lys Ile Xaa Phe Gly Thr His Ile
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 Ser Gly Arg Ile Ile Xaa Cys Ala Phe Thr Val Thr Phe Asn Pro Lys
 260 265 270
 Tyr Asp Ile Leu Leu Thr Ala Val Lys Asp Ala Thr Asn Thr Gly Ile
 275 280 285
 Lys Cys Ala Gly Ile Asp Val Arg Leu Cys Asp Val Gly Glu Ala Ile
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 Gln Glu Val Met Glu Ser Tyr Glu Val Glu Ile Asp Gly Lys Thr Tyr
 305 310 315 320
 Gln Val Lys Pro Ile Arg Asn Xaa Asn Gly Xaa Ser Ile Gly Pro Tyr
 325 330 335

Arg Xaa Xaa Ala Gly Lys Thr Val Pro Ile Val Lys Gly Gly Glu Ala
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 Thr Arg Met Glu Glu Gly Glu Val Tyr Ala Ile Xaa Thr Phe Gly Ser
 355 360 365
 Thr Gly Lys Gly Val Val His Asp Asp Met Glu Cys Ser His Tyr Met
 370 375 380
 Lys Asn Phe Asp Val Gly His Val Pro Ile Arg Leu Pro Arg Thr Lys
 385 390 395 400
 His Leu Leu Asn Val Ile Asn Glu Asn Phe Gly Thr Leu Ala Phe Cys
 405 410 415
 Arg Arg Trp Leu Asp Arg Leu Gly Glu Ser Lys Tyr Leu Met Ala Leu
 420 425 430
 Lys Asn Leu Cys Asp Leu Gly Ile Val Asp Pro Xaa Pro Pro Xaa Cys
 435 440 445
 Asp Ile Lys Gly Ser Tyr Thr Ala Gln Phe Xaa His Thr Ile Leu Leu
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 35 40 45
 Lys Lys Lys Lys Ser Asn Val Lys Lys Ile Glu Leu Leu Phe Pro Asp
 50 55 60
 Gly Lys Tyr Pro Glu Gly Ala Trp Met Asp Tyr His Gln Asp Phe Asn
 65 70 75 80
 Leu Gln Arg Thr Thr Asp Glu Glu Ser Arg Tyr Leu Lys Arg Asp Leu
 85 90 95
 Glu Arg Ala Glu His Trp Asn Asp Val Arg Lys Gly Ala Glu Ile His
 100 105 110

Arg Arg Val Arg Arg Ala Ile Lys Asp Arg Ile Val Pro Gly Met Lys
 115 120 125
 Leu Met Asp Ile Ala Asp Met Ile Glu Asn Thr Thr Arg Lys Tyr Thr
 130 135 140
 Gly Ala Glu Asn Leu Leu Ala Met Glu Asp Pro Lys Ser Gln Gly Ile
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 Gly Xaa Pro Thr Gly Leu Ser Leu Asn His Cys Ala Ala Xaa Phe Thr
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 Pro Asn Ala Gly Asp Lys Thr Val Leu Lys Tyr Glu Asp Val Met Lys
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 Val Xaa Tyr Gly Val Gln Val Asn Gly Asn Ile Ile Xaa Ser Ala Phe
 195 200 205
 Thr Val Ser Phe Asp Pro Gln Tyr Asp Asn Leu Leu Ala Ala Val Lys
 210 215 220
 Asp Ala Thr Tyr Thr Gly Ile Lys Glu Ala Gly Ile Asp Val Arg Leu
 225 230 235 240
 Thr Asp Ile Gly Glu Ala Ile Gln Glu Val Met Glu Ser Tyr Glu Val
 245 250 255
 Glu Ile Asn Gly Glu Thr Tyr Gln Val Lys Pro Cys Arg Asn Xaa Cys
 260 265 270
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 275 280 285
 Ile Val Lys Asn Gly Asp Thr Thr Lys Met Glu Glu Gly Glu His Phe
 290 295 300
 Ala Ile Xaa Thr Phe Gly Ser Thr Gly Arg Gly Tyr Val Thr Ala Gly
 305 310 315 320
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 Pro Thr Leu Asp Ser Ala Lys Asn Leu Leu Lys Thr Ile Asp Arg Asn
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 Phe Gly Thr Leu Pro Phe Cys Arg Arg Tyr Leu Asp Arg Leu Gly Gln
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 Glu Lys Tyr Leu Phe Ala Leu Asn Asn Leu Val Arg His Gly Leu Val
 370 375 380
 Gln Asp Xaa Pro Pro Xaa Asn Asp Ile Pro Gly Ser Tyr Thr Ala Gln
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ctgtttccag atggaaaagta ccagaaaggt gcgtggatgg actatcatca agatttcaat 240
ctgcaaaagaa ccacggatga agaatcacgt tatttgaaaa gggatctgga aagggccgaa 300
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gagacttacc aggttaaacc ttgtcgtaat ctatgtggcc acagtatcgc accatatcgt 840
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ttcgaacaca ccatcttgtt gcatgctcac aaaaaggaag tcgtttcgaa aggtgatgac 1260
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 35 40 45
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 50 55 60
 Asp Glu Val Ala Arg Gln Leu Glu Arg Ser Ala Leu Glu Asp Lys Glu
 65 70 75 80
 Arg Asp Glu Asp Asp Glu Asp Gly Asp Gly Asp Gly Ala Thr
 85 90 95
 Gly Lys Lys Lys Lys Lys Lys Lys Lys Arg Gly Pro Lys Val Gln
 100 105 110
 Thr Asp Pro Pro Ser Val Pro Ile Cys Asp Leu Tyr Pro Asn Gly Val
 115 120 125
 Phe Pro Lys Gly Gln Glu Cys Glu Tyr Pro Pro Thr Gln Asp Gly Arg
 130 135 140
 Thr Ala Ala Trp Arg Thr Thr Ser Glu Glu Lys Lys Ala Leu Asp Gln
 145 150 155 160
 Ala Ser Glu Glu Ile Trp Asn Asp Phe Arg Glu Ala Ala Glu Ala His
 165 170 175
 Arg Gln Val Arg Lys Tyr Val Met Ser Trp Ile Lys Pro Gly Met Thr
 180 185 190
 Met Ile Glu Ile Cys Glu Lys Leu Glu Asp Cys Ser Arg Lys Leu Ile
 195 200 205

Lys Glu Asn Gly Leu Asn Ala Gly Leu Ala Phe Pro Thr Gly Cys Ser
 210 215 220
 Leu Asn Asn Cys Ala Ala His Tyr Thr Pro Asn Ala Gly Asp Thr Thr
 225 230 235 240
 Val Leu Gln Tyr Asp Asp Ile Cys Lys Ile Asp Phe Gly Thr His Ile
 245 250 255
 Ser Gly Arg Ile Ile Asp Cys Ala Phe Thr Val Thr Phe Asn Pro Lys
 260 265 270
 Tyr Asp Thr Leu Leu Lys Ala Val Lys Asp Ala Thr Asn Thr Gly Ile
 275 280 285
 Lys Cys Ala Gly Ile Asp Val Arg Leu Cys Asp Val Gly Glu Ala Ile
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 Gln Glu Val Met Glu Ser Tyr Glu Val Glu Ile Asp Gly Lys Thr Tyr
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 Gln Val Lys Pro Ile Arg Asn Leu Asn Gly His Ser Ile Gly Gln Tyr
 325 330 335
 Arg Ile His Ala Gly Lys Thr Val Pro Ile Val Lys Gly Gly Glu Ala
 340 345 350
 Thr Arg Met Glu Glu Gly Glu Val Tyr Ala Ile Glu Thr Phe Gly Ser
 355 360 365
 Thr Gly Lys Gly Val Val His Asp Asp Met Glu Cys Ser His Tyr Met
 370 375 380
 Lys Asn Phe Asp Val Gly His Val Pro Ile Arg Leu Pro Arg Thr Lys
 385 390 395 400
 His Leu Leu Asn Val Ile Asn Glu Asn Phe Gly Thr Leu Ala Phe Cys
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Glu Ala Ala Lys Lys Lys Arg Arg Lys Lys Lys Lys Gly Lys Gly Ala
      35              40              45

Val Ser Ala Val Gln Gln Glu Leu Asp Lys Glu Ser Gly Ala Leu Val
      50              55              60

Asp Glu Val Ala Lys Gln Leu Glu Ser Gln Ala Leu Glu Glu Lys Glu
      65              70              75              80

Arg Asp Asp Asp Asp Glu Asp Gly Asp Gly Asp Ala Asp Gly Ala Thr
      85              90              95

Gly Lys Lys Lys Lys Lys Lys Lys Lys Lys Arg Gly Pro Lys Val Gln
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Thr Asp Pro Pro Ser Val Pro Ile Cys Asp Leu Tyr Pro Asn Gly Val
      115             120             125

Phe Pro Lys Gly Gln Glu Cys Glu Tyr Pro Pro Thr Gln Asp Gly Arg
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Ala Ser Glu Glu Ile Trp Asn Asp Phe Arg Glu Ala Ala Glu Ala His
      165             170             175

Arg Gln Val Arg Lys Tyr Val Met Ser Trp Ile Lys Pro Gly Met Thr
      180             185             190

Met Ile Glu Ile Cys Glu Lys Leu Glu Asp Cys Ser Arg Lys Leu Ile
      195             200             205

Lys Glu Asn Gly Leu Asn Ala Gly Leu Ala Phe Pro Thr Gly Cys Ser
      210             215             220

Leu Asn Asn Cys Ala Ala His Tyr Thr Pro Asn Ala Gly Asp Thr Thr
      225             230             235             240

Val Leu Gln Tyr Asp Asp Ile Cys Lys Ile Asp Phe Gly Thr His Ile
      245             250             255

Ser Gly Arg Ile Ile Asp Cys Ala Phe Thr Val Thr Phe Asn Pro Lys
      260             265             270

Tyr Asp Ile Leu Leu Thr Ala Val Lys Asp Ala Thr Asn Thr Gly Ile
      275             280             285

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Lys Cys Ala Gly Ile Asp Val Arg Leu Cys Asp Val Gly Glu Ala Ile
 290 295 300

Gln Glu Val Met Glu Ser Tyr Glu Val Glu Ile Asp Gly Lys Thr Tyr
 305 310 315 320

Gln Val Lys Pro Ile Arg Asn Leu Asn Gly His Ser Ile Gly Pro Tyr
 325 330 335

Arg Ile His Ala Gly Lys Thr Val Pro Ile Val Lys Gly Gly Glu Ala
 340 345 350

Thr Arg Met Glu Glu Gly Glu Val Tyr Ala Ile Glu Thr Phe Gly Ser
 355 360 365

Thr Gly Lys Gly Val Val His Asp Asp Met Glu Cys Ser His Tyr Met
 370 375 380

Lys Asn Phe Asp Val Gly His Val Pro Ile Arg Leu Pro Arg Thr Lys
 385 390 395 400

His Leu Leu Asn Val Ile Asn Glu Asn Phe Gly Thr Leu Ala Phe Cys
 405 410 415

Arg Arg Trp Leu Asp Arg Leu Gly Glu Ser Lys Tyr Leu Met Ala Leu
 420 425 430

Lys Asn Leu Cys Asp Leu Gly Ile Val Asp Pro Tyr Pro Pro Leu Cys
 435 440 445

Asp Ile Lys Gly Ser Tyr Thr Ala Gln Phe Glu His Thr Ile Leu Leu
 450 455 460

Arg Pro Thr Cys Lys Glu Val Val Ser Arg Gly Asp Asp Tyr
 465 470 475

<210> 14

<211> 437

<212> PRT

<213> *Saccharomyces* sp.

<220>

<223> Yeast MetAP2

<400> 14

Met Thr Asp Ala Glu Ile Glu Asn Ser Pro Ala Ser Asp Leu Lys Glu
 1 5 10 15

Leu Asn Leu Glu Asn Glu Gly Val Glu Gln Gln Asp Gln Ala Lys Ala
 20 25 30

Asp Glu Ser Asp Pro Val Glu Ser Lys Lys Lys Lys Asn Lys Lys Lys
 35 40 45

Lys Lys Lys Lys Ser Asn Val Lys Lys Ile Glu Leu Leu Phe Pro Asp
 50 55 60

Gly Lys Tyr Pro Glu Gly Ala Trp Met Asp Tyr His Gln Asp Phe Asn
 65 70 75 80
 Leu Gln Arg Thr Thr Asp Glu Glu Ser Arg Tyr Leu Lys Arg Asp Leu
 85 90 95
 Glu Arg Ala Glu His Trp Asn Asp Val Arg Lys Gly Ala Glu Ile His
 100 105 110
 Arg Arg Val Arg Arg Ala Ile Lys Asp Arg Ile Val Pro Gly Met Lys
 115 120 125
 Leu Met Asp Ile Ala Asp Met Ile Glu Asn Thr Thr Arg Lys Tyr Thr
 130 135 140
 Gly Ala Glu Asn Leu Leu Ala Met Glu Asp Pro Lys Ser Gln Gly Ile
 145 150 155 160
 Gly Phe Pro Thr Gly Leu Ser Leu Asn His Cys Ala Ala His Phe Thr
 165 170 175
 Pro Asn Ala Gly Asp Lys Thr Val Leu Lys Tyr Glu Asp Val Met Lys
 180 185 190
 Val Asp Tyr Gly Val Gln Val Asn Gly Asn Ile Ile Asp Ser Ala Phe
 195 200 205
 Thr Val Ser Phe Asp Pro Gln Tyr Asp Asn Leu Leu Ala Ala Val Lys
 210 215 220
 Asp Ala Thr Tyr Thr Gly Ile Lys Glu Ala Gly Ile Asp Val Arg Leu
 225 230 235 240
 Thr Asp Ile Gly Glu Ala Ile Gln Glu Val Met Glu Ser Tyr Glu Val
 245 250 255
 Glu Ile Asn Gly Glu Thr Tyr Gln Val Lys Pro Cys Arg Asn Leu Cys
 260 265 270
 Gly His Ser Ile Ala Pro Tyr Arg Ile His Gly Gly Lys Ser Val Pro
 275 280 285
 Ile Val Lys Asn Gly Asp Thr Thr Lys Met Glu Glu Gly Glu His Phe
 290 295 300
 Ala Ile Glu Thr Phe Gly Ser Thr Gly Arg Gly Tyr Val Thr Ala Gly
 305 310 315 320
 Gly Glu Val Ser His Tyr Ala Arg Ser Ala Glu Asp His Gln Val Met
 325 330 335
 Pro Thr Leu Asp Ser Ala Lys Asn Leu Leu Lys Thr Ile Asp Arg Asn
 340 345 350
 Phe Gly Thr Leu Pro Phe Cys Arg Arg Tyr Leu Asp Arg Leu Gly Gln
 355 360 365

Glu Lys Tyr Leu Phe Ala Leu Asn Asn Leu Val Arg His Gly Leu Val
 370 375 380

Gln Asp Tyr Pro Pro Leu Asn Asp Ile Pro Gly Ser Tyr Thr Ala Gln
 385 390 395 400

Phe Glu His Thr Ile Leu Leu His Ala His Lys Lys Glu Val Val Ser
 405 410 415

Lys Gly Asp Asp Tyr Gly Lys Met Arg Phe Gln Met Ala Ser Ser Leu
 420 425 430

Gly Ile Ile Leu Leu
 435

<210> 15
 <211> 71
 <212> PRT
 <213> Rattus sp.

<220>
 <223> Rat polylysine

<400> 15
 Lys Lys Lys Arg Arg Lys Lys Lys Lys Gly Lys Gly Ala Val Ser Ala
 1 5 10 15

Gly Gln Gln Glu Leu Asp Lys Glu Ser Gly Thr Ser Val Asp Glu Val
 20 25 30

Ala Lys Gln Leu Glu Arg Gln Ala Leu Glu Glu Lys Glu Lys Asp Asp
 35 40 45

Asp Asp Glu Asp Gly Asp Gly Asp Gly Asp Gly Ala Ala Gly Lys Lys
 50 55 60

Lys Lys Lys Lys Lys Lys Lys
 65 70

<210> 16
 <211> 480
 <212> PRT
 <213> Rattus sp.

<220>
 <223> Rat dnvMetAP2

<220>
 <221> SITE
 <222> (219)
 <223> May be any naturally occurring amino acid

<220>
 <221> SITE
 <222> (231)
 <223> May be any amino acid, except His

<220>
 <221> SITE
 <222> (251)
 <223> May be any naturally occurring amino acid

<220>
 <221> SITE
 <222> (262)
 <223> May be any naturally occurring amino acid

<220>
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 <222> (328)
 <223> May be any naturally occurring amino acid

<220>
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 <222> (331)
 <223> May be any naturally occurring amino acid

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 <222> (338)..(339)
 <223> May be any naturally occurring amino acid

<220>
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 <222> (364)
 <223> May be any naturally occurring amino acid

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 <222> (444)
 <223> May be any naturally occurring amino acid

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 <222> (447)
 <223> May be any naturally occurring amino acid

<220>
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 <222> (459)
 <223> May be any naturally occurring amino acid

<400> 16
 Met Ala Gly Val Glu Glu Ala Ser Ser Phe Gly Gly His Leu Asn Arg
 1 5 10 15
 Asp Leu Asp Pro Asp Asp Arg Glu Glu Gly Thr Ser Ser Thr Ala Glu
 20 25 30
 Glu Ala Ala Lys Lys Lys Arg Arg Lys Lys Lys Lys Gly Lys Gly Ala
 35 40 45
 Val Ser Ala Gly Gln Gln Glu Leu Asp Lys Glu Ser Gly Thr Ser Val
 50 55 60

Asp Glu Val Ala Lys Gln Leu Glu Arg Gln Ala Leu Glu Glu Lys Glu
 65 70 75 80
 Lys Asp Asp Asp Asp Glu Asp Gly Asp Gly Asp Gly Ala Ala
 85 90 95
 Gly Lys Lys Lys Lys Lys Lys Lys Lys Arg Gly Pro Arg Val Gln
 100 105 110
 Thr Asp Pro Pro Ser Val Pro Ile Cys Asp Leu Tyr Pro Asn Gly Val
 115 120 125
 Phe Pro Lys Gly Gln Glu Cys Glu Tyr Pro Pro Thr Gln Asp Gly Arg
 130 135 140
 Thr Ala Ala Trp Arg Thr Thr Ser Glu Glu Lys Lys Ala Leu Asp Gln
 145 150 155 160
 Ala Ser Glu Glu Ile Trp Asn Asp Phe Arg Glu Ala Ala Glu Ala His
 165 170 175
 Arg Gln Val Arg Lys Tyr Val Met Ser Trp Ile Lys Pro Gly Met Thr
 180 185 190
 Met Ile Glu Ile Cys Glu Lys Leu Glu Asp Cys Ser Arg Lys Leu Ile
 195 200 205
 Lys Glu Asn Gly Leu Asn Ala Gly Leu Ala Xaa Pro Thr Gly Cys Ser
 210 215 220
 Leu Asn Asn Cys Ala Ala Xaa Tyr Thr Pro Asn Ala Gly Asp Thr Thr
 225 230 235 240
 Val Leu Gln Tyr Asp Asp Ile Cys Lys Ile Xaa Phe Gly Thr His Ile
 245 250 255
 Ser Gly Arg Ile Ile Xaa Cys Ala Phe Thr Val Thr Phe Asn Pro Lys
 260 265 270
 Tyr Asp Ile Leu Leu Lys Ala Val Lys Asp Ala Thr Asn Thr Gly Ile
 275 280 285
 Lys Cys Ala Gly Ile Asp Val Arg Leu Cys Asp Val Gly Glu Ala Ile
 290 295 300
 Gln Glu Val Met Glu Ser Tyr Glu Val Glu Ile Asp Gly Lys Thr Tyr
 305 310 315 320
 Gln Val Lys Pro Ile Arg Asn Xaa Asn Gly Xaa Ser Ile Gly Pro Tyr
 325 330 335
 Arg Xaa Xaa Ala Gly Lys Thr Val Pro Ile Val Lys Gly Gly Glu Ala
 340 345 350
 Thr Arg Met Glu Glu Gly Glu Val Tyr Ala Ile Xaa Thr Phe Gly Ser
 355 360 365

Thr Gly Lys Gly Val Val His Asp Asp Met Glu Cys Ser His Tyr Met
370 375 380

Lys Asn Phe Asp Val Gly His Val Pro Ile Arg Leu Pro Arg Thr Lys
385 390 395 400

His Leu Leu Asn Val Ile Asn Glu Asn Phe Gly Thr Leu Ala Phe Cys
405 410 415

Arg Arg Trp Leu Asp Arg Leu Gly Glu Ser Lys Tyr Leu Met Ala Leu
420 425 430

Lys Asn Leu Cys Asp Leu Gly Ile Val Asp Pro Xaa Pro Pro Xaa Cys
435 440 445

Asp Ile Lys Gly Ser Tyr Thr Ala Gln Phe Xaa His Thr Ile Leu Cys
450 455 460

Ala Gln Pro Val Lys Lys Leu Ser Ala Glu Glu Met Thr Ile Lys Thr
465 470 475 480

<210> 17

<211> 480

<212> PRT

<213> Rattus sp.

<220>

<223> Rat MetAP2

<400> 17

Met Ala Gly Val Glu Glu Ala Ser Ser Phe Gly Gly His Leu Asn Arg
1 5 10 15

Asp Leu Asp Pro Asp Asp Arg Glu Glu Gly Thr Ser Ser Thr Ala Glu
20 25 30

Glu Ala Ala Lys Lys Lys Arg Arg Lys Lys Lys Lys Gly Lys Gly Ala
35 40 45

Val Ser Ala Gly Gln Gln Glu Leu Asp Lys Glu Ser Gly Thr Ser Val
50 55 60

Asp Glu Val Ala Lys Gln Leu Glu Arg Gln Ala Leu Glu Glu Lys Glu
65 70 75 80

Lys Asp Asp Asp Asp Glu Asp Gly Asp Gly Asp Gly Asp Gly Ala Ala
85 90 95

Gly Lys Lys Lys Lys Lys Lys Lys Lys Arg Gly Pro Arg Val Gln
100 105 110

Thr Asp Pro Pro Ser Val Pro Ile Cys Asp Leu Tyr Pro Asn Gly Val
115 120 125

Phe Pro Lys Gly Gln Glu Cys Glu Tyr Pro Pro Thr Gln Asp Gly Arg
130 135 140

Thr Ala Ala Trp Arg Thr Thr Ser Glu Glu Lys Lys Ala Leu Asp Gln
 145 150 155 160
 Ala Ser Glu Glu Ile Trp Asn Asp Phe Arg Glu Ala Ala Glu Ala His
 165 170 175
 Arg Gln Val Arg Lys Tyr Val Met Ser Trp Ile Lys Pro Gly Met Thr
 180 185 190
 Met Ile Glu Ile Cys Glu Lys Leu Glu Asp Cys Ser Arg Lys Leu Ile
 195 200 205
 Lys Glu Asn Gly Leu Asn Ala Gly Leu Ala Phe Pro Thr Gly Cys Ser
 210 215 220
 Leu Asn Asn Cys Ala Ala His Tyr Thr Pro Asn Ala Gly Asp Thr Thr
 225 230 235 240
 Val Leu Gln Tyr Asp Asp Ile Cys Lys Ile Asp Phe Gly Thr His Ile
 245 250 255
 Ser Gly Arg Ile Ile Asp Cys Ala Phe Thr Val Thr Phe Asn Pro Lys
 260 265 270
 Tyr Asp Ile Leu Leu Lys Ala Val Lys Asp Ala Thr Asn Thr Gly Ile
 275 280 285
 Lys Cys Ala Gly Ile Asp Val Arg Leu Cys Asp Val Gly Glu Ala Ile
 290 295 300
 Gln Glu Val Met Glu Ser Tyr Glu Val Glu Ile Asp Gly Lys Thr Tyr
 305 310 315 320
 Gln Val Lys Pro Ile Arg Asn Leu Asn Gly His Ser Ile Gly Pro Tyr
 325 330 335
 Arg Ile His Ala Gly Lys Thr Val Pro Ile Val Lys Gly Gly Glu Ala
 340 345 350
 Thr Arg Met Glu Glu Gly Glu Val Tyr Ala Ile Glu Thr Phe Gly Ser
 355 360 365
 Thr Gly Lys Gly Val Val His Asp Asp Met Glu Cys Ser His Tyr Met
 370 375 380
 Lys Asn Phe Asp Val Gly His Val Pro Ile Arg Leu Pro Arg Thr Lys
 385 390 395 400
 His Leu Leu Asn Val Ile Asn Glu Asn Phe Gly Thr Leu Ala Phe Cys
 405 410 415
 Arg Arg Trp Leu Asp Arg Leu Gly Glu Ser Lys Tyr Leu Met Ala Leu
 420 425 430
 Lys Asn Leu Cys Asp Leu Gly Ile Val Asp Pro Tyr Pro Pro Leu Cys
 435 440 445

Asp Ile Lys Gly Ser Tyr Thr Ala Gln Phe Glu His Thr Ile Leu Cys
 450 455 460

Ala Gln Pro Val Lys Lys Leu Ser Ala Glu Glu Met Thr Ile Lys Thr
 465 470 475 480

<210> 18
 <211> 1944
 <212> DNA
 <213> Rattus sp.

<220>
 <223> Rat MetAP2 variant

<220>
 <221> misc_feature
 <222> (779)
 <223> Any nucleotide

<400> 18
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 ctctctctct ttccctctcg ggcaacatgg cgggcgtgga agaggcatcg tctttcgggg 120
 gccacctgaa tcgcgacctg gatccagacg acaggggaaga gggaacctcc agcacggccg 180
 aggaagccgc caagaagaaa agacggaaga agaagaaggg caaaggggct gtgtcagcag 240
 ggcaacaaga acttgataaa gaatcgggaa cctcagtggg cgaagtagca aaacagttgg 300
 agagacaagc actggaggag aaagagaaa atgatgacga tgaagatgga gatggtgatg 360
 gtgatggtgc agctggggaag aagaagaaaa agaagaagaa gaagagagga ccaagagttc 420
 aaacagaccc tccctcagtt ccaatatgtg acctgtatcc taatggtgta tttcccaaag 480
 gacaagagtg tgaataccca cccacccaag atgggcggac agctgcttgg agaaccacaa 540
 gtgaagagaa aaaggcgcta gaccaggcta gtgaggagat ttggaacgac ttccgagaag 600
 ctgccgaagc acaccggcaa gttaggaaat acgtcatgag ctggatcaag cctgggatga 660
 caatgataga aatatgtgag aagttggaag actgttccc aaagctcata aaggagaatg 720
 ggtaaatgc aggcctggcc tttccactg ggtgttctct caacaactgt gctgcagcnt 780
 acactcccaa tgctggtgac acgacagtct tacagtacga cgacatctgt aagatcgact 840
 ttggaacgca tataagtggg agaataattg attgtgcttt tactgttact tttaatccca 900
 aatatgacat attattaaaa gctgtaaaa atgccaccaa tactggaata aagtgtgcgg 960
 ggattgacgt cgtctctgt gatgtcggcg aggccattca agaagttatg gagtccatg 1020
 aagtggaaat agatgggaag acctaccaag tgaacccat acgtaactta aatggacatt 1080
 caattgggccc atatagaatt catgctggaa aaacagtggc cattgtgaaa ggaggggaag 1140
 ctacaaggat ggaggaagga gaggtgtatg ccattgagac ctttggtagc acaggggaag 1200
 gcgtgggtca tgacgatatg gaatgttcac actacatgaa aaattttgat gtgggacacg 1260
 tgccaataag gcttccaaga acaaaacact tgttgaatgt catcaatgaa aactttggta 1320
 cccttgccct ctgccgaagg tggctggatc gcttgggaga aagtaaatat ttaatggctc 1380
 tgaagaacct gtgtgacttg ggcattgtag atccatatcc accactctgt gacattaaag 1440
 gatcatacac agcacagttt gaacatacca tactctgcgc ccaacctgta aagaagttgt 1500
 cagcagagga gatgactatt aaaacttagt ccaaagccaa ctcaacgtct ttattttcta 1560
 agctttgttg gaacacatta taccacaagt aatttgcaac atgtctgttt taacagtgga 1620
 cctgtgtaat gccgttatcc atgtttaaag gagtttgatc aaagccaaac tgtctacatg 1680
 taattaacca aggaaaaggc tttcaagact ttactgttaa ctgtttctcc cgtctaggaa 1740
 atgtgtact gtcactagt taggaattac ttaaacgttt tgttttgaag acctaaagaga 1800
 tgctttttgg atatttatat tgccatattc tacttggat gctttgaatg actacatata 1860
 tccagttctg cacctatgcc ctctggtatt gctttttaac cttcctggaa tccattttct 1920
 aaaaaataaa gacattttca gatc 1944

<210> 19
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 transit peptide

<400> 19
 Gly Arg Lys Lys Arg Arg Gln Arg
 1 5

<210> 20
 <211> 40
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 20
 gcgcaagctt atgattgaat tactgtttcc agatggaaag

40

<210> 21
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 21
 gcgcctcgag tcagtagtca tcacctttcg aaacg

35

<210> 22
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 22
 Cys Lys Glu Val Val Ser Lys Gly Asp Asp Tyr
 1 5 10

<210> 23
 <211> 9
 <212> PRT
 <213> Artificial Sequence


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<220>
<223> Description of Artificial Sequence: Synthetic
      peptide
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<400> 23
Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
1 5

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<210> 24
<211> 4
<212> PRT
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Synthetic
      peptide
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<400> 24
Met Gly Met Met
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<210> 25
<211> 63
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide
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[illegible]

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<210> 26
<211> 37
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

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<400> 26
cacagaattc cccgcatccc cagcatgcct gctattg
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